

0905

HCP

OIPE

RAW SEQUENCE LISTING

DATE: 09/10/2001

PATENT APPLICATION: US/09/783,320

TIME: 11:21:51

Input Set : A:\LEX-0137-USA SEQLIST.txt

Output Set: N:\CRF3\09102001\I783320.raw

4 <110> APPLICANT: Walke, D. Wade
 5 Hu, Yi
 6 Nepomichy, Boris
 7 Turner, C. Alexander Jr
 8 Zambrowicz, Brian
 11 <120> TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
 13 <130> FILE REFERENCE: LEX-0137-USA
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/783,320
 C--> 15 <141> CURRENT FILING DATE: 2001-02-15
 15 <150> PRIOR APPLICATION NUMBER: US 60/183,582
 16 <151> PRIOR FILING DATE: 2000-02-18
 18 <150> PRIOR APPLICATION NUMBER: US 60/184,014
 19 <151> PRIOR FILING DATE: 2000-02-22
 21 <160> NUMBER OF SEQ ID NOS: 50
 23 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 3108
 27 <212> TYPE: DNA
 28 <213> ORGANISM: homo sapiens
 30 <400> SEQUENCE: 1

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32	tcctatgatc	tccgcagttt	ggtgtctcg	ttatttaaaa	gaaatccat	ggatagacca	120
33	tcagtcaact	ccatattgga	gaaaggtttt	atagccaaac	gcattgaaaa	gtttctct	180
34	cctcagctta	ttgcagaaga	attttgtcta	aaaacatttt	cgaaggttgg	atcacagcct	240
35	ataccagcta	aaagaccagc	tccaggacaa	aactcgattt	ctgttatgcc	tgctcagaaaa	300
36	attacaaggc	ctgcccctaa	atatgaaata	cccttagcat	ataagaata	tggagataaaa	360
37	aaattacacg	aaaagaaaacc	actgcaaaaaa	cataaacagg	cccatcaaac	tccagagaag	420
38	agagtgaata	ctggagaaga	aaggaggaaa	atatctgagg	aagcagcaag	aaagagaagg	480
39	ctgaaattta	ttgaaaaaaa	aaagaaacaa	aaggatcaga	ttatttagtt	aatgaaggct	540
40	gaacaaatga	aaaggcaaga	aaagggaaagg	ttggaaagaa	taaatagggc	cagggAACAA	600
41	ggatggagaa	atgtgctaag	tgctggtgg	agtggtgaag	taaaggctcc	ttttctggc	660
42	agtggaggg	ctatagctcc	atcatcttt	tcttctcgag	gacagtatga	acattaccat	720
43	gccatttttg	accaaatgca	gcaacaaaga	gcagaagata	atgaagctaa	atggaaaaga	780
44	gaardatatg	gtcgaggct	tccagaaagg	caaaaaggc	agctagctgt	agaaagagct	840
45	aaacaagttag	aagagttct	gcagcggaaa	cggaaagcta	tgcagaataa	agctcgagcc	900
46	gaaggacata	tggaaatcct	gcaaaacctg	gcagctatgt	atggaggcag	gcccaagctct	960
47	tcaagaggag	ggaagccaag	aaacaaagag	gaagaggttt	atctggcaag	actgaggcaa	1020
48	ataagactac	agaatttcaa	tgagcgc当地	cagattaaag	ccaaacttcg	tggtaaaaag	1080
49	aaagaagcta	atcattctga	aggacaagaa	ggaagtgaag	aggctgacat	gaggcgcaaa	1140
50	aaaatcaat	cactgaaggc	ccatgcaat	gcacgtctg	ctgtactaaa	agaacaacta	1200
51	gaacgaaaga	gaaaggagc	ttatgagaga	gaaaaaaaaa	tgtggaaaga	gcatttgg	1260
52	gctaaaggag	ttaagagttc	tgatgttct	ccacctttgg	gacagcatga	aacaggtggc	1320
53	tctccatcaa	agcaacagat	gagatctgtt	atttctgtaa	cttcagcttt	gaaagaagtt	1380
54	ggcgtggaca	gtagtttaac	tgataccccg	gaaacttcag	aagagatgca	aaagaccaac	1440
55	aatgcttattt	caagtaagcg	agaaatactt	cgcagattaa	atgaaaatct	taaagctcaa	1500
56	gaagatgaaa	aaggaatgca	gaatctctct	gatactttt	agataaaatgt	tcatgaagat	1560
57	gccaagagc	atgaaaaaaa	aaaatcagtt	tcatctgatc	gcaagaatgt	ggaggcagga	1620

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58	ggtaacttg	tgattcctct	ggatgagtt	acactagata	catccttctc	tacaactgaa	1680
59	agacatacag	tggagaagt	tattaaatta	ggtcataatg	gatctccaag	aagagcctgg	1740
60	ggaaaaagtc	cgacagattc	tgttctaaag	atacttggag	aagctgaact	acaacttcag	1800
61	acagaactat	tagaaaatac	aactattaga	agttagattt	cacatgaaat	aaacccatca	1860
62	aaacccttaa	ttactggaga	aaaaaaagta	caatgtat	cacatgaaat	aaacccatca	1920
63	gctattgtt	atttcctgt	tgagacaaaa	agtcccagt	tcagtggaggc	atctccacag	1980
64	atgtcattga	aactggaagg	aaatttagaa	gaacctgtat	attingaaac	agaaattcta	2040
65	caagagccaa	gtgaaacaaa	caaagatgag	agcttgcct	gcactattac	tgtgtgtgg	2100
66	attagtgagg	aaaaagaaaac	aaaggaaact	cagtccgcag	ataggatcac	cattcaggaa	2160
67	aatgaagttt	ctgaagatgg	agtctcgagt	actgtggacc	aacttagtga	cattcatata	2220
68	gaggctggaa	ccatgattc	tcagcactct	aaatgtgtat	tagataagtc	tgtcaaccg	2280
69	gaaccat	tccataaggt	ggttcattct	gaacacttga	acttagtccc	tcaagtcaa	2340
70	tcagttcagt	gttcaccaga	agaatcctt	gcatttcgtat	ctcactcgca	tttaccacca	2400
71	aaaaataaaa	acaagaattc	cttgcgtatt	ggacttcaa	ctggctgtt	tgtgcaaac	2460
72	aacccaaaga	tgttaaggac	atgttca	ccagatctct	caaagctgtt	cagaaccctt	2520
73	atggatgtt	ccaccgtagg	agatgtcgt	caagacaatc	ttgaaataga	tgaaattaaa	2580
74	gataaaaaca	ttaaagaagg	accttctgtat	tctgaagaca	ttgtgtttga	agaaactgac	2640
75	acagatttac	aagagctgca	ggcctcgat	gaacagttac	ttagggaaaca	acctggtaa	2700
76	gaatacagtg	aagaagaaga	gtcagtctt	aagaacagtg	atgtggagcc	aactgcaa	2760
77	gggacagatg	tggcagatga	agatgacaat	cccagtagtg	aaagtgcct	gaacgaagaa	2820
78	tggcactcag	ataaacatgt	tgttggaaatt	gctgtgtat	gtgaatgcga	tagtgtctt	2880
79	aaccat	aggaaactgag	acttcatct	gagcaggaaa	tggctttga	aaaattctt	2940
80	gaggttat	agaaaataaa	ggctattcat	gaagatgaag	atggaaat	tgaaattttgt	3000
81	tcaaaaatag	ttcaaaaat	tttggaaat	gaacatcagc	atcttatgc	caagattctt	3060
82	catttagtca	tggcagatgg	agcctaccaa	gaagataatg	atgaataa		3108

84 <210> SEQ ID NO: 2

85 <211> LENGTH: 1035

86 <212> TYPE: PRT

87 <213> ORGANISM: homo sapiens

89 <400> SEQUENCE: 2

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91	1				5				10					15		
92	Ser	Leu	His	Tyr	Ser	Tyr	Asp	Leu	Arg	Ser	Leu	Val	Ser	Gln	Leu	Phe
93							20		25					30		
94	Lys	Arg	Asn	Pro	Arg	Asp	Arg	Pro	Ser	Val	Asn	Ser	Ile	Leu	Glu	Lys
95							35		40					45		
96	Gly	Phe	Ile	Ala	Lys	Arg	Ile	Glu	Lys	Phe	Leu	Ser	Pro	Gln	Leu	Ile
97							50		55					60		
98	Ala	Glu	Glu	Phe	Cys	Leu	Lys	Thr	Phe	Ser	Lys	Phe	Gly	Ser	Gln	Pro
99							65		70					75		80
100	Ile	Pro	Ala	Lys	Arg	Pro	Ala	Ser	Gly	Gln	Asn	Ser	Ile	Ser	Val	Met
101							85		90					95		
102	Pro	Ala	Gln	Lys	Ile	Thr	Lys	Pro	Ala	Ala	Lys	Tyr	Gly	Ile	Pro	Leu
103							100		105					110		
104	Ala	Tyr	Lys	Lys	Tyr	Gly	Asp	Lys	Lys	Leu	His	Glu	Lys	Lys	Pro	Leu
105							115		120					125		
106	Gln	Lys	His	Lys	Gln	Ala	His	Gln	Thr	Pro	Glu	Lys	Arg	Val	Asn	Thr
107							130		135					140		
108	Gly	Glu	Glu	Arg	Arg	Lys	Ile	Ser	Glu	Glu	Ala	Ala	Arg	Lys	Arg	Arg

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109	145	150	155	160
110	Leu Glu Phe Ile Glu Lys Glu Lys Lys Gln Lys Asp Gln Ile Ile Ser			
111		165	170	175
112	Leu Met Lys Ala Glu Gln Met Lys Arg Gln Glu Lys Glu Arg Leu Glu			
113		180	185	190
114	Arg Ile Asn Arg Ala Arg Glu Gln Gly Trp Arg Asn Val Leu Ser Ala			
115		195	200	205
116	Gly Gly Ser Gly Glu Val Lys Ala Pro Phe Leu Gly Ser Gly Gly Thr			
117		210	215	220
118	Ile Ala Pro Ser Ser Phe Ser Ser Arg Gly Gln Tyr Glu His Tyr His			
119		225	230	240
120	Ala Ile Phe Asp Gln Met Gln Gln Arg Ala Glu Asp Asn Glu Ala			
121		245	250	255
122	Lys Trp Lys Arg Glu Ile Tyr Gly Arg Gly Leu Pro Glu Arg Gln Lys			
123		260	265	270
124	Gly Gln Leu Ala Val Glu Arg Ala Lys Gln Val Glu Glu Phe Leu Gln			
125		275	280	285
126	Arg Lys Arg Glu Ala Met Gln Asn Lys Ala Arg Ala Glu Gly His Met			
127		290	295	300
128	Gly Ile Leu Gln Asn Leu Ala Ala Met Tyr Gly Gly Arg Pro Ser Ser			
129		305	310	320
130	Ser Arg Gly Gly Lys Pro Arg Asn Lys Glu Glu Glu Val Tyr Leu Ala			
131		325	330	335
132	Arg Leu Arg Gln Ile Arg Leu Gln Asn Phe Asn Glu Arg Gln Gln Ile			
133		340	345	350
134	Lys Ala Lys Leu Arg Gly Glu Lys Lys Glu Ala Asn His Ser Glu Gly			
135		355	360	365
136	Gln Glu Gly Ser Glu Glu Ala Asp Met Arg Arg Lys Lys Ile Glu Ser			
137		370	375	380
138	Leu Lys Ala His Ala Asn Ala Arg Ala Ala Val Leu Lys Glu Gln Leu			
139		385	390	395
140	Glu Arg Lys Arg Lys Glu Ala Tyr Glu Arg Glu Lys Lys Val Trp Glu			
141		405	410	415
142	Glu His Leu Val Ala Lys Gly Val Lys Ser Ser Asp Val Ser Pro Pro			
143		420	425	430
144	Leu Gly Gln His Glu Thr Gly Gly Ser Pro Ser Lys Gln Gln Met Arg			
145		435	440	445
146	Ser Val Ile Ser Val Thr Ser Ala Leu Lys Glu Val Gly Val Asp Ser			
147		450	455	460
148	Ser Leu Thr Asp Thr Arg Glu Thr Ser Glu Glu Met Gln Lys Thr Asn			
149		465	470	475
150	Asn Ala Ile Ser Ser Lys Arg Glu Ile Leu Arg Arg Leu Asn Glu Asn			
151		485	490	495
152	Leu Lys Ala Gln Glu Asp Glu Lys Gly Met Gln Asn Leu Ser Asp Thr			
153		500	505	510
154	Phe Glu Ile Asn Val His Glu Asp Ala Lys Glu His Glu Lys Glu Lys			
155		515	520	525
156	Ser Val Ser Ser Asp Arg Lys Lys Trp Glu Ala Gly Gly Gln Leu Val			
157		530	535	540

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158 Ile Pro Leu Asp Glu Leu Thr Leu Asp Thr Ser Phe Ser Thr Thr Glu
 159 545 550 555 560
 160 Arg His Thr Val Gly Glu Val Ile Lys Leu Gly Pro Asn Gly Ser Pro
 161 565 570 575
 162 Arg Arg Ala Trp Gly Lys Ser Pro Thr Asp Ser Val Leu Lys Ile Leu
 163 580 585 590
 164 Gly Glu Ala Glu Leu Gln Leu Gln Thr Glu Leu Leu Glu Asn Thr Thr
 165 595 600 605
 166 Ile Arg Ser Glu Ile Ser Pro Glu Gly Glu Lys Tyr Lys Pro Leu Ile
 167 610 615 620
 168 Thr Gly Glu Lys Lys Val Gln Cys Ile Ser His Glu Ile Asn Pro Ser
 169 625 630 635 640
 170 Ala Ile Val Asp Ser Pro Val Glu Thr Lys Ser Pro Glu Phe Ser Glu
 171 645 650 655
 172 Ala Ser Pro Gln Met Ser Leu Lys Leu Glu Gly Asn Leu Glu Glu Pro
 173 660 665 670
 174 Asp Asp Leu Glu Thr Glu Ile Leu Gln Glu Pro Ser Gly Thr Asn Lys
 175 675 680 685
 176 Asp Glu Ser Leu Pro Cys Thr Ile Thr Asp Val Trp Ile Ser Glu Glu
 177 690 695 700
 178 Lys Glu Thr Lys Glu Thr Gln Ser Ala Asp Arg Ile Thr Ile Gln Glu
 179 705 710 715 720
 180 Asn Glu Val Ser Glu Asp Gly Val Ser Ser Thr Val Asp Gln Leu Ser
 181 725 730 735
 182 Asp Ile His Ile Glu Pro Gly Thr Asn Asp Ser Gln His Ser Lys Cys
 183 740 745 750
 184 Asp Val Asp Lys Ser Val Gln Pro Glu Pro Phe Phe His Lys Val Val
 185 755 760 765
 186 His Ser Glu His Leu Asn Leu Val Pro Gln Val Gln Ser Val Gln Cys
 187 770 775 780
 188 Ser Pro Glu Glu Ser Phe Ala Phe Arg Ser His Ser His Leu Pro Pro
 189 785 790 795 800
 190 Lys Asn Lys Asn Lys Asn Ser Leu Leu Ile Gly Leu Ser Thr Gly Leu
 191 805 810 815
 192 Phe Asp Ala Asn Asn Pro Lys Met Leu Arg Thr Cys Ser Leu Pro Asp
 193 820 825 830
 194 Leu Ser Lys Leu Phe Arg Thr Leu Met Asp Val Pro Thr Val Gly Asp
 195 835 840 845
 196 Val Arg Gln Asp Asn Leu Glu Ile Asp Glu Ile Lys Asp Glu Asn Ile
 197 850 855 860
 198 Lys Glu Gly Pro Ser Asp Ser Glu Asp Ile Val Phe Glu Glu Thr Asp
 199 865 870 875 880
 200 Thr Asp Leu Gln Glu Leu Gln Ala Ser Met Glu Gln Leu Leu Arg Glu
 201 885 890 895
 202 Gln Pro Gly Glu Glu Tyr Ser Glu Glu Glu Ser Val Leu Lys Asn
 203 900 905 910
 204 Ser Asp Val Glu Pro Thr Ala Asn Gly Thr Asp Val Ala Asp Glu Asp
 205 915 920 925
 206 Asp Asn Pro Ser Ser Glu Ser Ala Leu Asn Glu Glu Trp His Ser Asp

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207	930	935	940	
208	Asn Ser Asp Gly Glu Ile Ala Ser Glu Cys Glu Cys Asp Ser Val Phe			
209	945	950	955	960
210	Asn His Leu Glu Glu Leu Arg Leu His Leu Glu Gln Glu Met Gly Phe			
211	965	970	975	
212	Glu Lys Phe Phe Glu Val Tyr Glu Lys Ile Lys Ala Ile His Glu Asp			
213	980	985	990	
214	Glu Asp Glu Asn Ile Glu Ile Cys Ser Lys Ile Val Gln Asn Ile Leu			
215	995	1000	1005	
216	Gly Asn Glu His Gln His Leu Tyr Ala Lys Ile Leu His Leu Val Met			
217	1010	1015	1020	
218	Ala Asp Gly Ala Tyr Gln Glu Asp Asn Asp Glu			
219	1025	1030	1035	
221	<210> SEQ ID NO: 3			
222	<211> LENGTH: 3645			
223	<212> TYPE: DNA			
224	<213> ORGANISM: homo sapiens			
226	<400> SEQUENCE: 3			
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229	tccagtaaag aaagagaaga atcaaggaga gaagttgcag tattggcaaa catgaagcat		180	
230	ccaaatatttgc tccagtatag agaatcattt gaagaaaatg gctctctcta catagtaatg		240	
231	gattactgtg agggagggaa tctgtttaag cgaataaaatg ctcagaaagg cggtttgttt		300	
232	caagaggatc agattttggaa ctgtttgtt cagatatgtt tggccctgaa acatgtacat		360	
233	gatagaaaaaa ttcttcatcg agacattaaa tctcagaaca tatttttaac taaagatgaa		420	
234	acagtacaac ttggagattt tggattgtt agagttctt atagtactgt agagctggct		480	
235	cgaacttgca tagggcccccc atactacttg tcacctgaaa tctgtaaaaa caaaccttac		540	
236	ataataaaaaa gtgacatttgc ggctctgggg tgtgtcctt atgagctgt tacacttaaa		600	
237	catgcttttgc aagctggcag tataaaaac ctggtactga agataatatc tggatctttt		660	
238	ccacctgtgt ctttgattt ttccatgtatgc ctccgcagg tgggtctca gtattttaaa		720	
239	agaaatcccta gggatagacc atcagtcaac tccatattgg agaaagggtt tatagccaaa		780	
240	cgcattgaaa agtttctctc tcctcagttt attgcagaag aattttgtct aaaaacattt		840	
241	tcgaagtttgc gatcacagcc tataccagct aaaagaccat cttcaggaca aaactcgatt		900	
242	tctgttatgc ctgctcagaa aattacaaag cctgcgcata aatatggaaat accttttagca		960	
243	tataagaaat atggagataa aaaattacac gaaaagaaac cactgcaaaa acataaacag		1020	
244	gcccatcaaa ctccagagaa gagagtgaat actggagaag aaaggaggaa aatatctgag		1080	
245	gaagcagcaa gaaagagaag gctggattt attgaaaaag aaaagaaaca aaaggatcag		1140	
246	attatttagtt taatgaaggc tgaacaaatg aaaaggcaag aaaaggaaag gtggaaaga		1200	
247	ataaataggg ccagggaca aggatggaga aatgtgttgc tgcgttgtt aagtgggtgaa		1260	
248	gtaaaggctc cttttctggg cagttgggg actatagctc catcatcttt ttcttcgcga		1320	
249	ggacagtatg aacattacca tgccattttt gaccaaatgc agcaacaaag agcagaagat		1380	
250	aatgaagcta aatggaaaaag agaaatataat ggtcgagggtc ttccagaaag gcaaaaagg		1440	
251	cagctagctg tagaaagagc taaaacaatgtt gaagagttcc tgcagcgaaa acgggaagct		1500	
252	atgcagaata aagctcgagc cgaaggacat atggtttatac tggcaagact gaggcaata		1560	
253	agactacaga atttcaatgtt ggcggcaacag attaaagcca aacttcgtgg tgaaaaagaaa		1620	
254	gaagctaatttctgtt acaagaaggtt agtgaagagg ctgacatgag ggcggcaaaaa		1680	
255	atcgaatcac tgaaggccca tgccaaatgc cgtgtgtt tactaaaaga acaactagaa		1740	
256	cgaaagagaa aggaggctt tgagagagaa aaaaaagttt gggaaagagca ttgggtggct		1800	
257	aaaggagtttta agagttctgtt tgtttctcca ctttggac agcatgaaac aggtggctt		1860	

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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date